#2

RAW SEQUENCE LISTING   DATE: 07/05/2001
PATENT APPLICATION: US/09/882,774   TIME: 11:25:37

Input Set : A:\003592-007.ST25.txt
Output Set: N:\CRF3\07052001\I882774.raw

```
   4 <110> APPLICANT: Houston, Michael E.
   5        Hodges, Robert
   7 <120> TITLE OF INVENTION: Use of Coiled-Coil Structural Scaffold to Generate
   8        Structure-Specific Peptides
  10 <130> FILE REFERENCE: 003592-007
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/882,774
C--> 12 <141> CURRENT FILING DATE: 2001-06-14
  12 <150> PRIOR APPLICATION NUMBER: US 60/211,892
  13 <151> PRIOR FILING DATE: 2000-06-14
  15 <150> PRIOR APPLICATION NUMBER: US 60/213,387
  16 <151> PRIOR FILING DATE: 2000-06-23
  18 <160> NUMBER OF SEQ ID NOS: 16
  20 <170> SOFTWARE: PatentIn version 3.0
  22 <210> SEQ ID NO: 1
  23 <211> LENGTH: 619
  24 <212> TYPE: PRT
  25 <213> ORGANISM: Streptococcus pneumoniae
  27 <400> SEQUENCE: 1
  29 Met Asn Lys Lys Lys Met Ile Leu Thr Ser Leu Ala Ser Val Ala Ile
  30 1               5                  10                  15
  32 Leu Gly Ala Gly Phe Val Ala Ser Gln Pro Thr Val Val Arg Ala Glu
  33              20                  25                  30
  35 Glu Ser Pro Val Ala Ser Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala
  36          35                  40                  45
  38 Ala Lys Lys Asp Ala Lys Asn Ala Lys Lys Ala Val Glu Asp Ala Gln
  39      50                  55                  60
  41 Lys Ala Leu Asp Asp Ala Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp
  42 65                  70                  75                  80
  44 Gln Lys Lys Thr Glu Glu Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu
  45              85                  90                  95
  47 Glu Met Asp Lys Ala Val Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr
  48              100                 105                 110
  50 Gln Gln Ala Thr Asp Lys Ala Ala Lys Asp Ala Ala Asp Lys Met Ile
  51          115                 120                 125
  53 Asp Glu Ala Lys Lys Arg Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr
  54      130                 135                 140
  56 Val Arg Ala Met Val Val Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys
  57 145                 150                 155                 160
  59 Lys Lys Ser Glu Glu Ala Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys
  60              165                 170                 175
  62 Leu Glu Glu Ala Lys Ala Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr
  63              180                 185                 190
  65 Glu Ala Lys Gln Lys Val Asp Ala Glu Glu Val Ala Pro Gln Ala Lys
  66          195                 200                 205
  68 Ile Ala Glu Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu Lys
  69      210                 215                 220
  71 Glu Ile Asp Glu Ser Glu Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg
```

see page 5

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```
72 225                    230                235                240
74 Ala Pro Leu Gln Ser Lys Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys
75                   245                250                255
77 Leu Glu Glu Leu Ser Asp Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala
78                   260                265                270
80 Lys Leu Glu Asp Gln Leu Lys Ala Ala Glu Glu Asn Asn Asn Val Glu
81        275                280                285
83 Asp Tyr Phe Lys Glu Gly Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala
84        290                295                300
86 Glu Leu Glu Lys Thr Glu Ala Asp Leu Lys Lys Ala Val Asn Glu Pro
87 305                310                315                320
89 Glu Lys Pro Ala Pro Ala Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala
90                   325                330                335
92 Glu Gln Pro Lys Pro Ala Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys
93        340                345                350
95 Pro Glu Lys Pro Ala Glu Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln
96        355                360                365
98 Gln Ala Glu Glu Asp Tyr Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg
99    370                375                380
101 Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro
102 385                390                395                400
104 Lys Thr Gly Trp Lys Gln Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr
105                   405                410                415
107 Asp Gly Ser Met Ala Thr Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr
108        420                425                430
110 Tyr Leu Asn Ser Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn
111        435                440                445
113 Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp
114    450                455                460
116 Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met
117 465                470                475                480
119 Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala
120        485                490                495
122 Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr
123        500                505                510
125 Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn
126        515                520                525
128 Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp
129    530                535                540
131 Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met
132 545                550                555                560
134 Ala Thr Gly Trp Val Lys Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala
135        565                570                575
137 Ser Gly Ala Met Lys Ala Ser Gln Trp Phe Lys Val Ser Asp Lys Trp
138        580                585                590
140 Tyr Tyr Val Asn Gly Leu Gly Ala Leu Ala Val Asn Thr Thr Val Asp
141        595                600                605
143 Gly Tyr Lys Val Asn Ala Asn Gly Glu Trp Val
144    610                615
```

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```
     147 <210> SEQ ID NO: 2
     148 <211> LENGTH: 40
     149 <212> TYPE: PRT
     150 <213> ORGANISM: Artificial Sequence
     152 <220> FEATURE:
     153 <223> OTHER INFORMATION: stabilizing strand
     155 <220> FEATURE:
     156 <221> NAME/KEY: MOD_RES
     157 <222> LOCATION: (2)
     158 <223> OTHER INFORMATION: Nle
     160 <400> SEQUENCE: 2
W--> 162 Cys Xaa Gly Gly Gly Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala
     163 1               5                   10              15
     165 Leu Lys Lys Glu Ile Glu Ala Leu Lys Lys Glu Ile Glu Ala Leu Lys
     166             20                  25                  30
     168 Lys Glu Ile Glu Ala Leu Lys Lys
     169         35                  40
     171 <210> SEQ ID NO: 3
     172 <211> LENGTH: 38
     173 <212> TYPE: PRT
     174 <213> ORGANISM: Artificial Sequence
     176 <220> FEATURE:
     177 <223> OTHER INFORMATION: hybrid sequence
     179 <220> FEATURE:
     180 <221> NAME/KEY: MOD_RES
     181 <222> LOCATION: (2)
     182 <223> OTHER INFORMATION: Nle
     184 <400> SEQUENCE: 3
W--> 186 Cys Xaa Gly Ile Glu Glu Leu Glu Lys Lys Ile Thr Glu Leu Lys Gln
     187 1               5                   10              15
     189 Lys Ile Asp Ala Leu Glu Asn Gln Ile His Arg Leu Glu Gln Glu Ile
     190             20                  25                  30
     192 Lys Glu Leu Asp Glu Ser
     193         35
     195 <210> SEQ ID NO: 4
     196 <211> LENGTH: 38
     197 <212> TYPE: PRT
     198 <213> ORGANISM: Artificial Sequence
     200 <220> FEATURE:
     201 <223> OTHER INFORMATION: hybrid sequence
     203 <220> FEATURE:
     204 <221> NAME/KEY: MOD_RES
     205 <222> LOCATION: (2)
     206 <223> OTHER INFORMATION: Nle
     208 <400> SEQUENCE: 4
W--> 210 Cys Xaa Gly Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln
     211 1               5                   10              15
     213 Lys Val Asp Ala Leu Glu Asn Gln Val His Arg Leu Glu Gln Glu Leu
     214             20                  25                  30
```

```
216 Lys Glu Ile Asp Glu Ser
217           35
219 <210> SEQ ID NO: 5
220 <211> LENGTH: 20
221 <212> TYPE: PRT
222 <213> ORGANISM: Artificial Sequence
224 <220> FEATURE:
225 <223> OTHER INFORMATION: consensus sequence
227 <220> FEATURE:
228 <221> NAME/KEY: PEPTIDE
229 <222> LOCATION: (4)..(20)
230 <223> OTHER INFORMATION: Amino acids 4, 5, 12, 16 and 20 are Xaa wherein Xaa = any
amino
231           acid
233 <400> SEQUENCE: 5
```

W--> 235 Glu Glu Leu Xaa Xaa Lys Ile Asp Glu Leu Asp Xaa Glu Ile Ala Xaa

```
236 1               5                       10                  15
```

W--> 238 Leu Glu Lys Xaa

```
239                20
241 <210> SEQ ID NO: 6
242 <211> LENGTH: 8
243 <212> TYPE: PRT
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: consensus sequence
249 <400> SEQUENCE: 6
251 Glu Glu Leu Ser Asp Lys Ile Asp
252 1               5
254 <210> SEQ ID NO: 7
255 <211> LENGTH: 27
256 <212> TYPE: PRT
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: hybrid sequence
262 <220> FEATURE:
263 <221> NAME/KEY: MOD_RES
264 <222> LOCATION: (2)
265 <223> OTHER INFORMATION: Nle
267 <400> SEQUENCE: 7
```

W--> 269 Cys Xaa Gly Glu Ile Glu Ala Leu Lys Lys Lys Ile Glu Glu Leu Ser

```
270 1               5                       10                  15
272 Asp Lys Ile Asp Glu Leu Glu Lys Glu Ile Lys
273                20                       25
275 <210> SEQ ID NO: 8
276 <211> LENGTH: 21
277 <212> TYPE: PRT
278 <213> ORGANISM: Haemophilus influenzae
280 <400> SEQUENCE: 8
282 Ile Lys Lys Val Leu Glu Ile Gly Leu Asn Met Ser Gln Glu Ala Ser
283 1               5                       10                  15
```

```
285 Asn Leu Thr Ser Ala
286             20
288 <210> SEQ ID NO: 9
289 <211> LENGTH: 27
290 <212> TYPE: PRT
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: hybrid sequence
296 <400> SEQUENCE: 9
298 Glu Ala Glu Ile Lys Lys Leu Leu Glu Ile Ile Leu Asn Leu Ser Gln
299 1               5               10              15
301 Glu Ile Ser Asn Leu Thr Ser Ala Leu Lys Gly
302             20                  25
304 <210> SEQ ID NO: 10
305 <211> LENGTH: 20
306 <212> TYPE: PRT
307 <213> ORGANISM: Streptococcus pneumoniae
309 <400> SEQUENCE: 10
311 Leu Glu Lys Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Gln Ala
312 1               5               10              15
314 Glu Gln Val Leu
315             20
317 <210> SEQ ID NO: 11
318 <211> LENGTH: 15
319 <212> TYPE: PRT
320 <213> ORGANISM: Streptococcus pneumoniae
322 <400> SEQUENCE: 11
324 Leu Glu Asp Asn Leu Lys Asp Ala Glu Thr Asn Asn Val Glu Asp
325 1               5               10              15
327 <210> SEQ ID NO: 12
328 <211> LENGTH: 10
329 <212> TYPE: PRT
330 <213> ORGANISM: Streptococcus pneumoniae
332 <400> SEQUENCE: 12
334 Leu Ala Lys Lys Gln Thr Glu Leu Glu Lys
335 1               5                   10
337 <210> SEQ ID NO: 13
338 <211> LENGTH: 35
339 <212> TYPE: PRT
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: hybrid sequence
345 <400> SEQUENCE: 13
347 Asp Val Glu Asp Phe Lys Asn Ser Asp Gly Glu Leu Glu Asp Asn Leu
348 1               5               10              15
350 Lys Asp Ala Glu Thr Asn Asn Val Glu Asp Ala Lys Lys Gln Thr Glu
351             20                  25                  30
353 Leu Glu Lys
354             35
```

FYF.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

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```
L:12  M:270 C: Current Application Number differs, Replaced Current Application No
L:12  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:162 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
```